

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/517-220

Source:

PCT

Date Processed by STIC:

5-19-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/517,220

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics-
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 1 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers:
 use space characters, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa. and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file. resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 07/19/2005

PATENT APPLICATION: US/10/517,220

TIME: 08:58:58

Input Set : E:\24615-20244.00 - seq list.txt

Output Set: N:\CRF4\07192005\J517220.raw

3 <110> APPLICANT: Edens, Luppo
 4 Lopez, Michel
 6 <120> TITLE OF INVENTION: Improved method for the prevention or reduction of haze in
 7 beverages
 9 <130> FILE REFERENCE: 246152024400
 11 <140> CURRENT APPLICATION NUMBER: US 10/517,220
 C--> 12 <141> CURRENT FILING DATE: 2004-12-07
 14 <150> PRIOR APPLICATION NUMBER: PCT/NL03/00352
 15 <151> PRIOR FILING DATE: 2003-05-14
 17 <150> PRIOR APPLICATION NUMBER: NL 02100681.2
 18 <151> PRIOR FILING DATE: 2002-06-07
 20 <160> NUMBER OF SEQ ID NOS: 7
 22 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed
 (Pg. 1-5) ←

ERRORED SEQUENCES

260 <210> SEQ ID NO: 4
 261 <211> LENGTH: 526
 262 <212> TYPE: PRT
 263 <213> ORGANISM: Aspergillus niger
 265 <400> SEQUENCE: 4
 266 Met Arg Ser Phe Ser Val Val Ala Ala Ala Ser Leu Ala Leu Ser Trp
 E--> 267 1 5 10 15
 268 Ala Ser Leu Ala Gln Ala Ala Arg Pro Arg Leu Val Pro Lys Pro Ile
 E--> 269 20 25 30
 270 Ser Arg Pro Ala Ser Ser Lys Ser Ala Ala Thr Thr Gly Glu Ala Tyr
 E--> 271 35 40 45
 272 Phe Glu Gln Leu Leu Asp His His Asn Pro Glu Lys Gly Thr Phe Ser
 E--> 273 50 55 60
 274 Gln Arg Tyr Trp Trp Ser Thr Glu Tyr Trp Gly Gly Pro Gly Ser Pro
 E--> 275 65 70 75 80
 276 Val Val Leu Phe Asn Pro Gly Glu Val Ser Ala Asp Gly Tyr Glu Gly
 E--> 277 85 90 95
 278 Tyr Leu Thr Asn Asp Thr Leu Thr Gly Val Tyr Ala Gln Glu Ile Gln
 E--> 279 100 105 110
 280 Gly Ala Val Ile Leu Ile Glu His Arg Tyr Trp Gly Asp Ser Ser Pro
 E--> 281 115 120 125
 282 Tyr Glu Val Leu Asn Ala Glu Thr Leu Gln Tyr Leu Thr Leu Asp Gln
 E--> 283 130 135 140
 284 Ser Ile Leu Asp Met Thr Tyr Phe Ala Glu Thr Val Lys Leu Gln Phe
 E--> 285 145 150 155 160
 286 Asp Asn Ser Ser Arg Ser Asn Ala Gln Asn Ala Pro Trp Val Met Val

← pls
 See item
 #3 on
 error
 Summary
 Sheet.

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Input Set : E:\24615-20244.00 - seq list.txt

Output Set: N:\CRF4\07192005\J517220.raw

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E--> 287   165       170   175
      288 Gly Gly Ser Tyr Ser Gly Ala Leu Thr Ala Trp Thr Glu Ser Ile Ala
E--> 289       180   185       190
      290 Pro Gly Thr Phe Trp Ala Tyr His Ala Thr Ser Ala Pro Val Glu Ala
E--> 291   195       200   205
      292 Ile Tyr Asp Phe Trp Gln Tyr Phe Tyr Pro Ile Gln Gln Gly Met Ala
E--> 293       210   215       220
      294 Gln Asn Cys Ser Lys Asp Val Ser Leu Val Ala Glu Tyr Val Asp Lys
E--> 295  225       230   235       240
      296 Ile Gly Lys Asn Gly Thr Ala Lys Glu Gln Gln Glu Leu Lys Glu Leu
E--> 297       245       250   255
      298 Phe Gly Leu Gly Ala Val Glu His Tyr Asp Asp Phe Ala Ala Val Leu
E--> 299       260   265       270
      300 Pro Asn Gly Pro Tyr Leu Trp Gln Asp Asn Asp Phe Val Thr Gly Tyr
E--> 301  275       280   285
      302 Ser Ser Phe Phe Gln Phe Cys Asp Ala Val Glu Gly Val Glu Ala Gly
E--> 303       290   295       300
      304 Ala Ala Val Thr Pro Gly Pro Glu Gly Val Gly Leu Glu Lys Ala Leu
E--> 305  305       310   315       320
      306 Ala Asn Tyr Ala Asn Trp Phe Asn Ser Thr Ile Leu Pro Asn Tyr Cys
E--> 307  325       330   335
      308 Ala Ser Tyr Gly Tyr Trp Thr Asp Glu Trp Ser Val Ala Cys Phe Asp
E--> 309       340   345       350
      310 Ser Tyr Asn Ala Ser Ser Pro Ile Phe Thr Asp Thr Ser Val Gly Asn
E--> 311  355       360   365
      312 Pro Val Asp Arg Gln Trp Glu Trp Phe Leu Cys Asn Glu Pro Phe Phe
E--> 313       370   375       380
      314 Trp Trp Gln Asp Gly Ala Pro Glu Gly Thr Ser Thr Ile Val Pro Arg
E--> 315  385       390   395       400
      316 Leu Val Ser Ala Ser Tyr Trp Gln Arg Gln Cys Pro Leu Tyr Phe Pro
E--> 317  405       410   415
      318 Glu Val Asn Gly Tyr Thr Tyr Gly Ser Ala Lys Gly Lys Asn Ser Ala
E--> 319       420   425       430
      320 Thr Val Asn Ser Trp Thr Gly Gly Trp Asp Met Thr Arg Asn Thr Thr
E--> 321  435       440   445
      322 Arg Leu Ile Trp Thr Asn Gly Gln Tyr Asp Pro Trp Arg Asp Ser Gly
E--> 323       450   455       460
      324 Val Ser Ser Thr Phe Arg Pro Gly Gly Pro Leu Val Ser Thr Ala Asn
E--> 325  465       470   475       480
      326 Glu Pro Val Gln Ile Ile Pro Gly Gly Phe His Cys Ser Asp Leu Tyr
E--> 327  485       490   495
      328 Met Glu Asp Tyr Tyr Ala Asn Glu Gly Val Arg Lys Val Val Asp Asn
E--> 329       500   505       510
      330 Glu Val Lys Gln Ile Lys Glu Trp Val Glu Glu Tyr Tyr Ala
E--> 331  515       520       525
      333 <210> SEQ ID NO: 5
      334 <211> LENGTH: 526
      335 <212> TYPE: PRT
      336 <213> ORGANISM: Aspergillus niger

```

< PLS
 see item
 # 3 on
 error
 Summary
 Sheet

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DATE: 07/19/2005

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Input Set : E:\24615-20244.00 - seq list.txt

Output Set: N:\CRF4\07192005\J517220.raw

338 <400> SEQUENCE: 5
339 Met Arg Ala Phe Ser Ala Val Ala Ala Ala Leu Ala Leu Ser Trp
E--> 340 1 5 10 15
341 Ala Ser Leu Ala Gln Ala Ala Arg Pro Arg Leu Val Pro Lys Pro Val
E--> 342 20 25 30
343 Ser Arg Pro Ala Ser Ser Lys Ser Ala Ala Thr Thr Gly Glu Ala Tyr
E--> 344 35 40 45
345 Phe Glu Gln Leu Leu Asp His His Asn Pro Glu Lys Gly Thr Phe Ser
E--> 346 50 55 60
347 Gln Arg Tyr Trp Trp Ser Thr Glu Tyr Trp Gly Gly Pro Gly Ser Pro
E--> 348 65 70 75 80
349 Val Val Leu Phe Thr Pro Gly Glu Val Ser Ala Asp Gly Tyr Glu Gly
E--> 350 85 90 95
351 Tyr Leu Thr Asn Gly Thr Leu Thr Gly Val Tyr Ala Gln Glu Ile Gln
E--> 352 100 105 110
353 Gly Ala Val Ile Leu Ile Glu His Arg Tyr Trp Gly Asp Ser Ser Pro
E--> 354 115 120 125
355 Tyr Glu Val Leu Asn Ala Glu Thr Leu Gln Tyr Leu Thr Leu Asp Gln
E--> 356 130 135 140
357 Ala Ile Leu Asp Met Thr Tyr Phe Ala Glu Thr Val Lys Leu Gln Phe
E--> 358 145 150 155 160
359 Asp Asn Ser Thr Arg Ser Asn Ala Gln Asn Ala Pro Trp Val Met Val
E--> 360 165 170 175
361 Gly Gly Ser Tyr Ser Gly Ala Leu Thr Ala Trp Thr Glu Ser Val Ala
E--> 362 180 185 190
363 Pro Gly Thr Phe Trp Ala Tyr His Ala Thr Ser Ala Pro Val Glu Ala
E--> 364 195 200 205
365 Ile Tyr Asp Tyr Trp Gln Tyr Phe Tyr Pro Ile Gln Gln Gly Met Ala
E--> 366 210 215 220
367 Gln Asn Cys Ser Lys Asp Val Ser Leu Val Ala Glu Tyr Val Asp Lys
E--> 368 225 230 235 240
369 Ile Gly Lys Asn Gly Thr Ala Lys Glu Gln Gln Ala Leu Lys Glu Leu
E--> 370 245 250 255
371 Phe Gly Leu Gly Ala Val Glu His Phe Asp Asp Phe Ala Ala Val Leu
E--> 372 260 265 270
373 Pro Asn Gly Pro Tyr Leu Trp Gln Asp Asn Asp Phe Ala Thr Gly Tyr
E--> 374 275 280 285
375 Ser Ser Phe Phe Gln Phe Cys Asp Ala Val Glu Gly Val Glu Ala Gly
E--> 376 290 295 300
377 Ala Ala Val Thr Pro Gly Pro Glu Gly Val Gly Leu Glu Lys Ala Leu
E--> 378 305 310 315 320
379 Ala Asn Tyr Ala Asn Trp Phe Asn Ser Thr Ile Leu Pro Asp Tyr Cys
E--> 380 325 330 335
381 Ala Ser Tyr Gly Tyr Trp Thr Asp Glu Trp Ser Val Ala Cys Phe Asp
E--> 382 340 345 350
383 Ser Tyr Asn Ala Ser Ser Pro Ile Tyr Thr Asp Thr Ser Val Gly Asn
E--> 384 355 360 365
385 Ala Val Asp Arg Gln Trp Glu Trp Phe Leu Cys Asn Glu Pro Phe Phe
E--> 386 370 375 380

-same
error

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Input Set : E:\24615-20244.00 - seq list.txt

Output Set: N:\CRF4\07192005\J517220.raw

387 Tyr Trp Gln Asp Gly Ala Pro Glu Gly Thr Ser Thr Ile Val Pro Arg
 E--> 388 385 390 395 400
 389 Leu Val Ser Ala Ser Tyr Trp Gln Arg Gln Cys Pro Leu Tyr Phe Pro
 E--> 390 405 410 415
 391 Glu Thr Asn Gly Tyr Thr Tyr Gly Ser Ala Lys Gly Lys Asn Ala Ala
 E--> 392 420 425 430
 393 Thr Val Asn Ser Trp Thr Gly Gly Trp Asp Met Thr Arg Asn Thr Thr
 E--> 394 435 440 445
 395 Arg Leu Ile Trp Thr Asn Gly Gln Tyr Asp Pro Trp Arg Asp Ser Gly
 E--> 396 450 455 460
 397 Val Ser Ser Thr Phe Arg Pro Gly Gly Pro Leu Ala Ser Thr Ala Asn
 E--> 398 465 470 475 480
 399 Glu Pro Val Gln Ile Ile Pro Gly Gly Phe His Cys Ser Asp Leu Tyr
 E--> 400 485 490 495
 401 Met Ala Asp Tyr Tyr Ala Asn Glu Gly Val Lys Lys Val Val Asp Asn
 E--> 402 500 505 510
 403 Glu Val Lys Gln Ile Lys Glu Trp Val Glu Glu Tyr Tyr Ala
 E--> 404 515 520 525
 464 <210> SEQ ID NO: 7
 465 <211> LENGTH: 516
 466 <212> TYPE: PRT
 467 <213> ORGANISM: Aspergillus niger
 469 <400> SEQUENCE: 7
 470 Met Arg Ser Phe Ser Val Val Ala Ala Ala Ser Leu Ala Leu Ser Trp
 E--> 471 1 5 10 15
 472 Ala Ser Leu Ala Gln Ala Ala Arg Pro Arg Leu Val Pro Lys Pro Ile
 E--> 473 20 25 30
 474 Ser Arg Pro Ala Ser Ser Lys Ser Ala Ala Thr Thr Gly Glu Ala Tyr
 E--> 475 35 40 45
 476 Phe Glu Gln Leu Leu Asp His His Asn Pro Glu Lys Gly Thr Phe Ser
 E--> 477 50 55 60
 478 Gln Arg Tyr Trp Trp Ser Thr Glu Tyr Trp Gly Gly Pro Gly Ser Pro
 E--> 479 65 70 75 80
 480 Val Val Leu Phe Asn Pro Gly Glu Val Ser Ala Asp Gly Tyr Glu Gly
 E--> 481 85 90 95
 482 Tyr Leu Thr Asn Asp Thr Leu Thr Gly Val Tyr Ala Gln Glu Ile Gln
 E--> 483 100 105 110
 484 Gly Ala Val Ile Leu Ile Glu His Arg Tyr Trp Gly Asp Ser Ser Pro
 E--> 485 115 120 125
 486 Tyr Glu Val Leu Asn Ala Glu Thr Leu Gln Tyr Leu Thr Leu Asp Gln
 E--> 487 130 135 140
 488 Ser Ile Leu Asp Met Thr Tyr Phe Ala Glu Thr Val Lys Leu Gln Phe
 E--> 489 145 150 155 160
 490 Asp Asn Ser Ser Arg Ser Asn Ala Gln Asn Ala Pro Trp Val Met Val
 E--> 491 165 170 175
 492 Gly Gly Ser Tyr Ser Gly Ala Leu Thr Ala Trp Thr Glu Ser Ile Ala
 E--> 493 180 185 190
 494 Pro Gly Thr Phe Trp Ala Tyr His Ala Thr Ser Ala Pro Val Glu Ala
 E--> 495 195 200 205

Same
 errors

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TIME: 08:58:58

Input Set : E:\24615-20244.00 - seq list.txt

Output Set: N:\CRF4\07192005\J517220.raw

496 Ile Tyr Asp Phe Gln Gly Met Ala Gln Asn Cys Ser Lys Asp Val Ser
E--> 497 210 215 220
498 Leu Val Ala Glu Tyr Val Asp Lys Ile Gly Lys Asn Gly Thr Ala Lys
E--> 499 225 230 235 240
500 Glu Gln Gln Glu Leu Lys Glu Leu Phe Gly Leu Gly Ala Val Glu His
E--> 501 245 250 255
502 Tyr Asp Asp Phe Ala Ala Val Leu Pro Asn Gly Pro Tyr Leu Trp Gln
E--> 503 260 265 270
504 Asp Asn Asp Phe Val Thr Gly Tyr Ser Ser Phe Phe Gln Phe Cys Asp
E--> 505 275 280 285
506 Ala Val Glu Gly Val Glu Ala Gly Ala Ala Val Thr Pro Gly Pro Glu
E--> 507 290 295 300
508 Gly Val Gly Leu Glu Lys Ala Leu Ala Asn Tyr Ala Asn Trp Phe Asn
E--> 509 305 310 315 320
510 Ser Thr Ile Leu Pro Asn Tyr Cys Ala Ser Tyr Gly Tyr Trp Thr Asp
E--> 511 325 330 335
512 Glu Trp Ser Val Ala Cys Phe Asp Ser Tyr Asn Ala Ser Ser Pro Ile
E--> 513 340 345 350
514 Phe Thr Asp Thr Ser Val Gly Asn Pro Val Asp Arg Gln Trp Glu Trp
E--> 515 355 360 365
516 Phe Leu Cys Asn Glu Pro Phe Phe Trp Trp Gln Asp Gly Ala Pro Glu
E--> 517 370 375 380
518 Gly Thr Ser Thr Ile Val Pro Arg Leu Val Ser Ala Ser Tyr Trp Gln
E--> 519 385 390 395 400
520 Arg Gln Cys Pro Leu Tyr Phe Pro Glu Val Asn Gly Tyr Thr Tyr Gly
E--> 521 405 410 415
522 Ser Ala Lys Gly Lys Asn Ser Ala Thr Val Asn Ser Trp Thr Gly Gly
E--> 523 420 425 430
524 Trp Asp Met Thr Arg Asn Thr Thr Arg Leu Ile Trp Thr Asn Gly Gln
E--> 525 435 440 445
526 Tyr Asp Pro Trp Arg Asp Ser Gly Val Ser Ser Thr Phe Arg Pro Gly
E--> 527 450 455 460
528 Gly Pro Leu Val Ser Thr Ala Asn Glu Pro Val Gln Ile Ile Pro Gly
E--> 529 465 470 475 480
530 Gly Phe His Cys Ser Asp Leu Tyr Met Glu Asp Tyr Tyr Ala Asn Glu
E--> 531 485 490 495
532 Gly Val Arg Lys Val Val Asp Asn Glu Val Lys Gln Ile Lys Glu Tyr
E--> 533 500 505 510
534 Gly Tyr Gly Cys
E--> 535 515

- Same
error

VERIFICATION SUMMARY

DATE: 07/19/2005

PATENT APPLICATION: US/10/517,220

TIME: 08:58:59

Input Set : E:\24615-20244.00 - seq list.txt

Output Set: N:\CRF4\07192005\J517220.raw

. L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
, L:267 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
' M:332 Repeated in SeqNo=4
L:340 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:471 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7